

09/890463

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BASPOC3.pap

1 SVIAKQMTYK VYMSGTVNGH YFEVEGDGKG KPYEGEQTVR LAVTKGGPLP
51 FAWDILSPQC QYGSIPFTKY PEDIPDYVKQ SFPGRYTWER IMNFEDGAVC
101 TVSNDSSIQG NCFIYHVKFS GLNFPPNGPV MQKKTQGWEP NTERLFARDG
151 MLIGNNFMAL KLEGGGHYLC EFKSTYKARK PVKMPGYHYV DRKLDVTNHN
201 KDYTSVEQRE ISIARKPLVA CCFFRVKSRH K* (SEQ IN NO: 3)

In bold, differences between clones.

Figure 3

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BASPOC4.pep

1 SVIAKQMTYK VYMSGTVNGH YFEVEGDGKG KPYEGEQTVR LAVTKGGPLP
51 FAWDILSPQC QYGSIPFTKY PEDIPDYVKQ SFPGRYTWER IMNFEDGAVC
101 TVSNDSSIQG NCFIYHVKFS GLNFPPNGPV MQKKTQGWEP NTERLFARDG
151 MLIGNNFMAL KLEGGGHYLC EFKSTYKAKK PVKMPGYHYV DRKLDVTNHN
201 KDYTSVEQCE ISIARKPVVA CRFFRVKSRH KYAVA* (SEQ ID NO: 4)

Figure 4

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t7SP6BASPOC3 Length: 841

1	TCCGTTATCG	CTAAACAGAT	GACCTACAAA	GTTTATATGT	CAGGCACGGT
51	CAATGGACAC	TACTTTGAGG	TCGAAGGCGA	TGGAAAAGGA	AAGCCTTACG
101	AGGGGGAGCA	GACGGTAAGG	CTGGCTGTCA	CCAAGGGCGG	ACCTCTGCCA
151	TTTGCTTGGG	ATATTTTATC	ACCACAGTGT	CAGTACGGAA	GCATACCATT
201	CACCAAGTAC	CCTGAAGACA	TCCCTGACTA	TGTAAAGCAG	TCATTCCCCG
251	GGAGATATAC	ATGGGAGAGG	ATCATGAACT	TTGAAGATGG	TGCAGTGTGT
301	ACTGTCAGCA	ATGATTCCAG	CATCCAAGGC	AACTGTTTCA	TCTACCATGT
351	CAAGTTCTCT	GGTTTGAAC	TTCTTCCCAA	TGGACCTGTT	ATGCAGAAGA
401	AGACACAGGG	CTGGGAACCC	AACACTGAGC	GTCTCTTTGC	ACGAGATGGA
451	ATGCTGATAG	GAAACAACCT	TATGGCTCTG	AAGTTAGAAG	GAGGTGGTCA
501	CTATTTGTGT	GAATTCAAAT	CTACTTACAA	GGCAAGGAAG	CCTGTGAAGA
551	TGCCAGGGTA	TCACTATGTT	GACCGCAAAC	TGGATGTAAC	CAATCACAAAC
601	AAGGATTACA	CTTCCGTGTA	GCAGCGTGAA	ATTTCATTG	CACGCAAACC
651	TTTGGTCGCC	TGCTGTTTTT	TCAGAGTCAA	ATCAAGGCAC	AAATAAGCAG
701	TGGCGTAAAA	AACGTAGATT	CTGATTTTAG	CTTAGAGAAG	TAGGAACGAA
751	GAAGTGTAGA	CAACCTTCAA	TGATTAAACT	TTTGAAAACA	ACSCCAAAAA
801	AAAAAAAAAA	AAAAAAAAAA	AAAAAGCGGC	CGCTCGAATT	A (SEQ ID NO: 5)

663 either A or C
In bold differences

Figure 5

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T7SP6BASPOC4 Length: 841 (today) Check: 7145 ..

1	TCCGTTATCG	CTAAACAGAT	GACCTACAAA	GTTTATATGT	CAGGCACGGT
51	CAATGGACAC	TACTTTGAGG	TCCAAGGCGA	TGGAAAAGGA	AAGCCTTACG
101	AGGGGGAGCA	GACGGTAAGG	CTGGCTGTCA	CCAAGGGCGG	ACCTCTGCCA
151	TTTGCTTGGG	ATATTTTATC	ACCACAGTGT	CAGTACGGAA	GCATACCATT
201	CACCAAGTAC	CCTGAAGACA	TCCCTGACTA	TGTAAAGCAG	TCATTCCCGG
251	GGAGATATAC	ATGGGAGAGG	ATCATGAACT	TTGAAGATGG	TGCAGTGTGT
301	ACTGTCAGCA	ATGATTCCAG	CATCCAAGGC	AACTGTTTCA	TCTACCATGT
351	CAAGTCTCT	GGTTTGAACT	TTCCTCCCAA	TGGACCTGTT	ATGCAGAAGA
401	AGACACAGGG	CTGGGAACCC	AACACTGAGC	GTCTCTTTGC	ACGAGATGGA
451	ATGCTGATAG	GAAACAACCT	TATGGCTCTG	AAGTTAGAAG	GAGGTGGTCA
501	CTATTTGTGT	GAATTCAAAT	CTACTTACAA	GGCAAAGAAG	CCTGTGAAGA
551	TGCCAGGGTA	TCACTATGTT	GACCGCAAAC	TGGATGTAAC	CAATCACAAC
601	AAGGATTACA	CTTCCGTTGA	GCAGTGTGAA	ATTTCCATTG	CACGCAAACC
651	TGTGGTCGCC	TGCCGTTTTT	TCAGAGTCAA	ATCAAGGCAC	AAATACGCAG
701	TGGCGTAAAA	AACGTAGATT	CTGATTTTAG	CTTATAGAAG	TAGGAACGAA
751	GAAGTGTAAG	CAACCATTAA	TGATTAAACT	TTTGAAAACA	ACGCCATAAA
801	AAAAAAAAAA	AAAAAAAAAA	AAAAAGCGGC	CGCTCGAATT	A (SEQ ID NO: 6)

Figure 6

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COLORED PROTEIN VECTOR

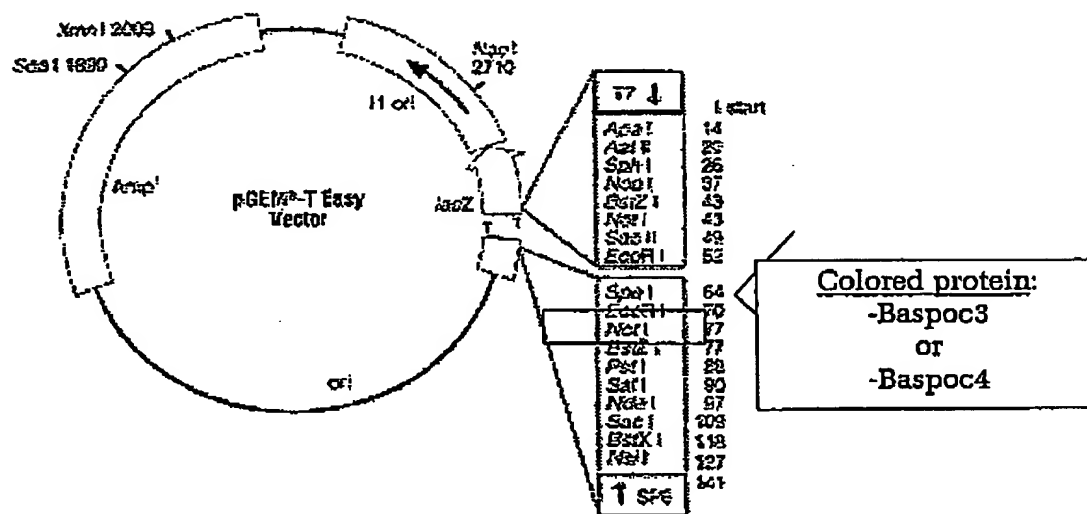


Figure 7

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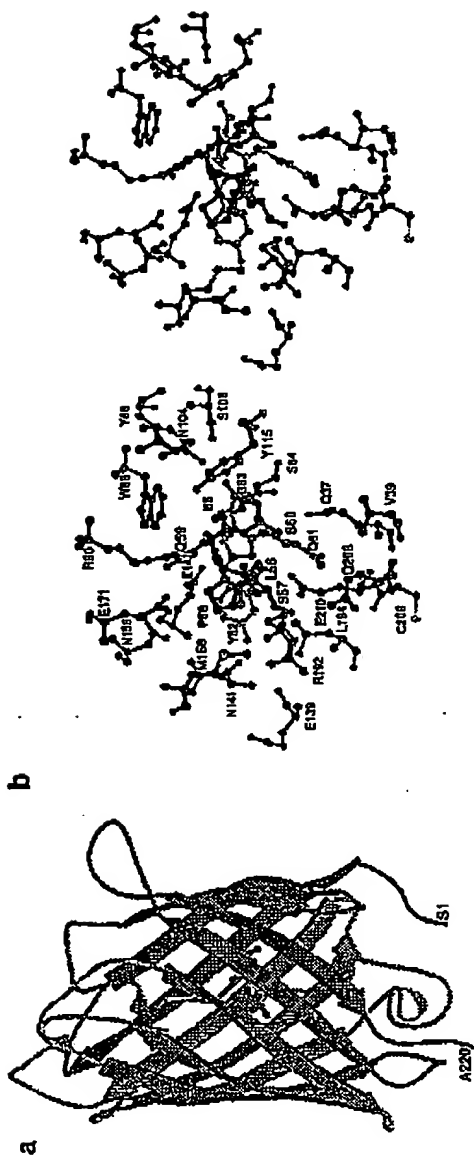


Figure 8

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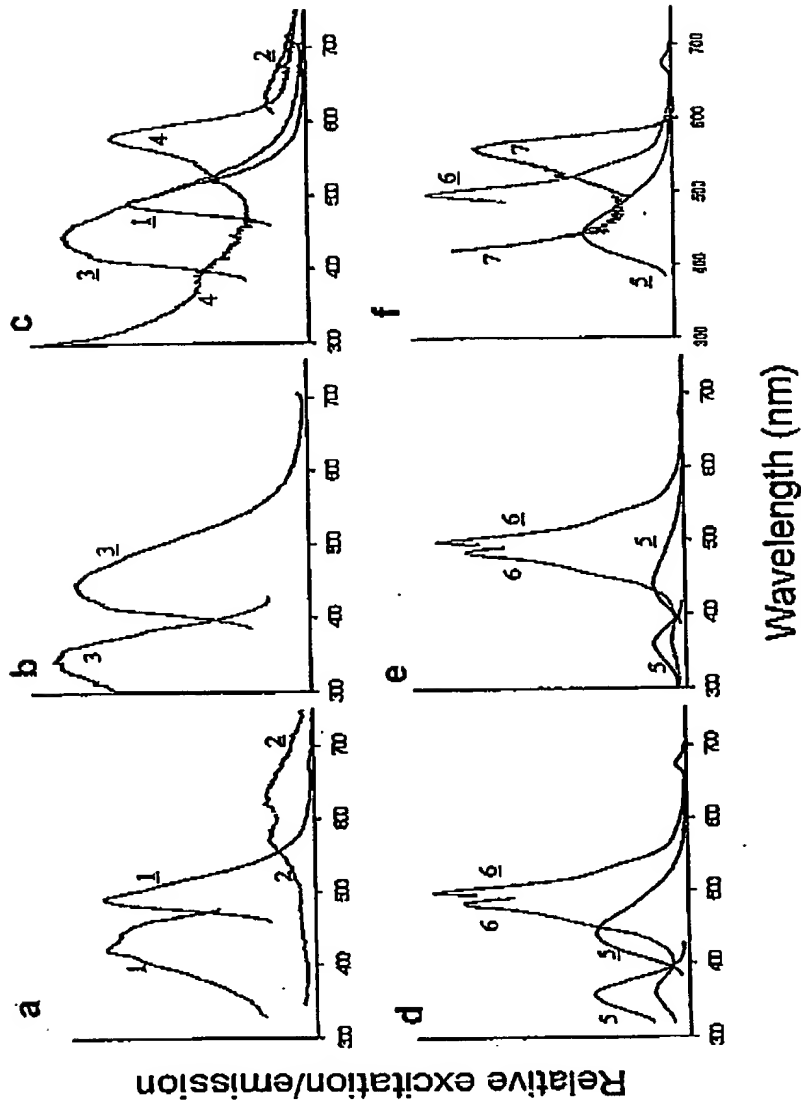


Figure 9

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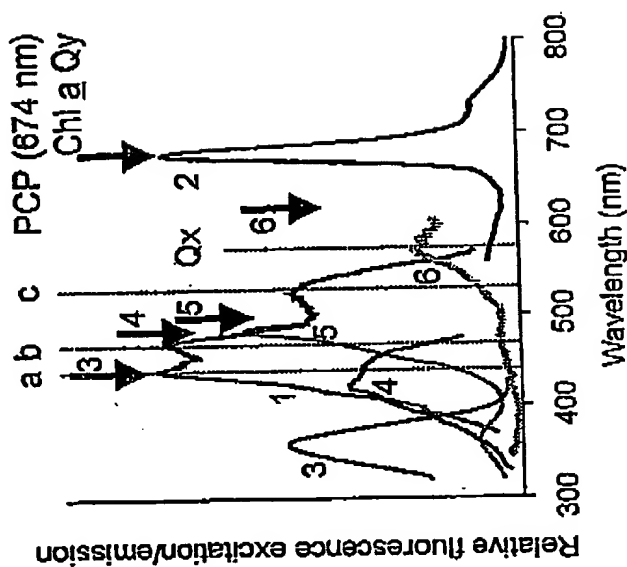


Figure 10